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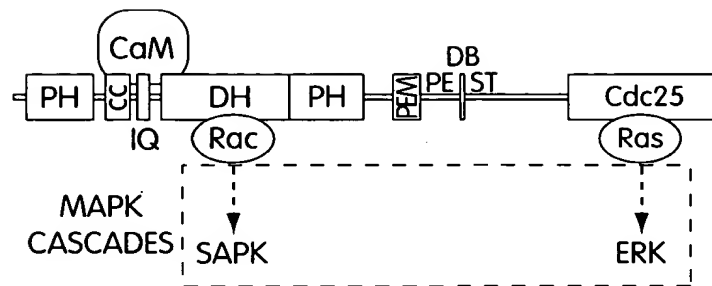


Fig. 1A

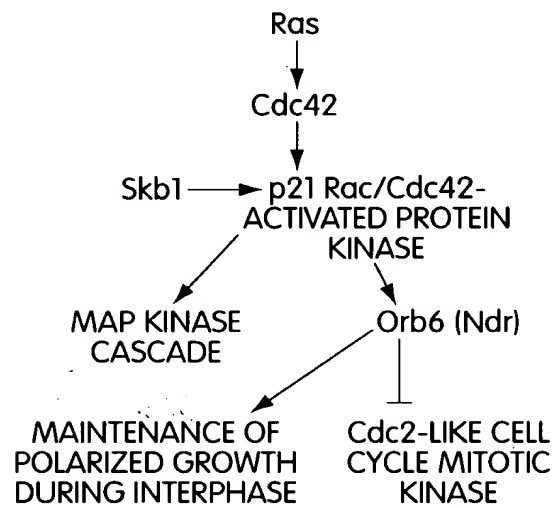


Fig. 1B

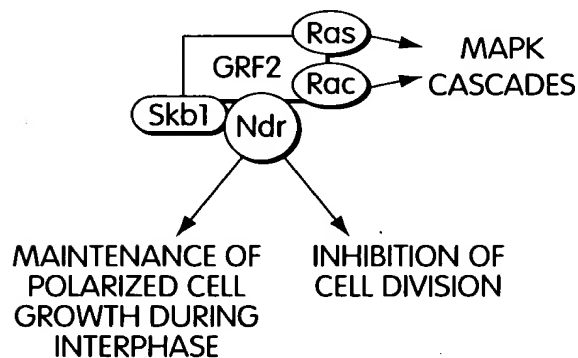


Fig. 1C

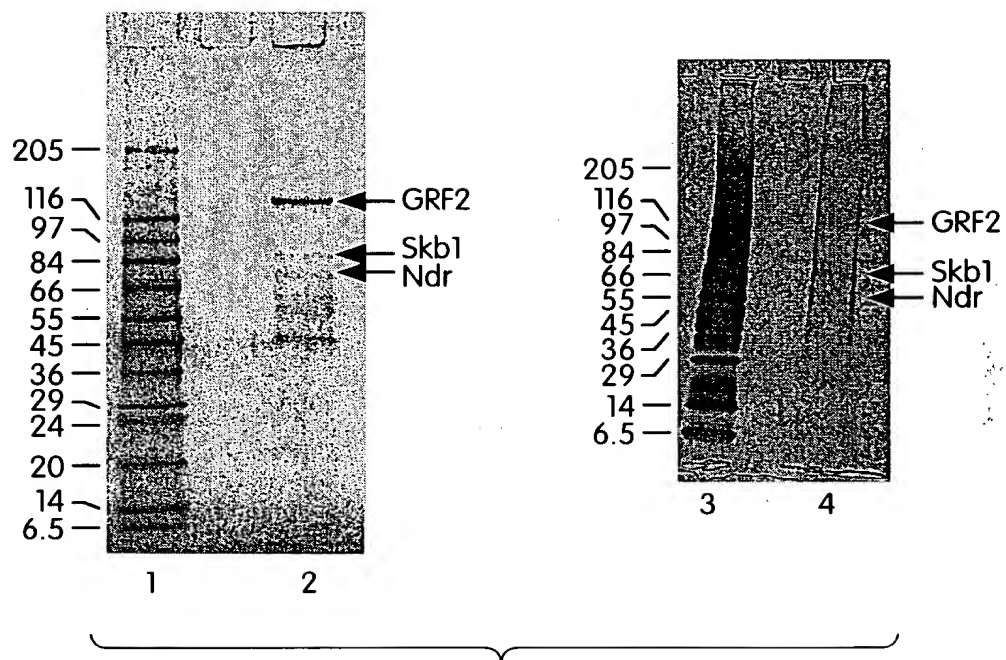


Fig. 2

PEPTIDE 40 (NUM. HITS = 92)

(1.0) GTVLDQVPVNPSLYLIK (17.0)

SYMBOL	MASS	a	a - 17	b	b - 17	y	y - 17
G, Gly	57.021	30.034	13.032	58.029	41.027	1856.053	1839.051
T, Thr	101.048	131.082	114.079	159.077	142.074	1799.032	1782.029
V, Val	99.068	230.150	213.148	258.145	241.143	1697.984	1680.981
L, Leu	113.084	343.235	326.232	371.229	354.227	1598.916	1581.913
D, Asp	115.027	458.261	441.259	486.256	469.254	1485.832	1468.829
Q, Gln	128.059	586.320	569.317	614.315	597.312	1370.805	1353.802
V, Val	99.068	685.388	668.386	713.383	696.381	1242.746	1225.743
P, Pro	97.053	782.441	765.439	810.436	793.433	1143.678	1126.675
V, Val	99.068	881.510	864.507	909.505	892.502	1046.625	1029.622
N, Asn	114.043	995.553	978.550	1023.547	1006.545	947.557	930.554
P, Pro	97.053	1092.605	1075.603	1120.600	1103.598	833.514	816.511
S, Ser	87.032	1179.637	1162.635	1207.632	1190.630	736.461	719.458
L, Leu	113.084	1292.721	1275.719	1320.716	1303.714	649.429	632.426
Y, Tyr	163.063	1455.785	1438.782	1483.780	1466.777	536.345	519.342
L, Leu	113.084	1568.869	1551.866	1596.864	1579.861	373.282	356.279
I, Ile	113.084	1681.953	1664.950	1709.948	1692.945	260.197	243.195
K, Lys	128.095	1810.048	1793.045	1838.043	1821.040	147.113	130.111

+TOF PRODUCT: FROM 928.5

7.10e1

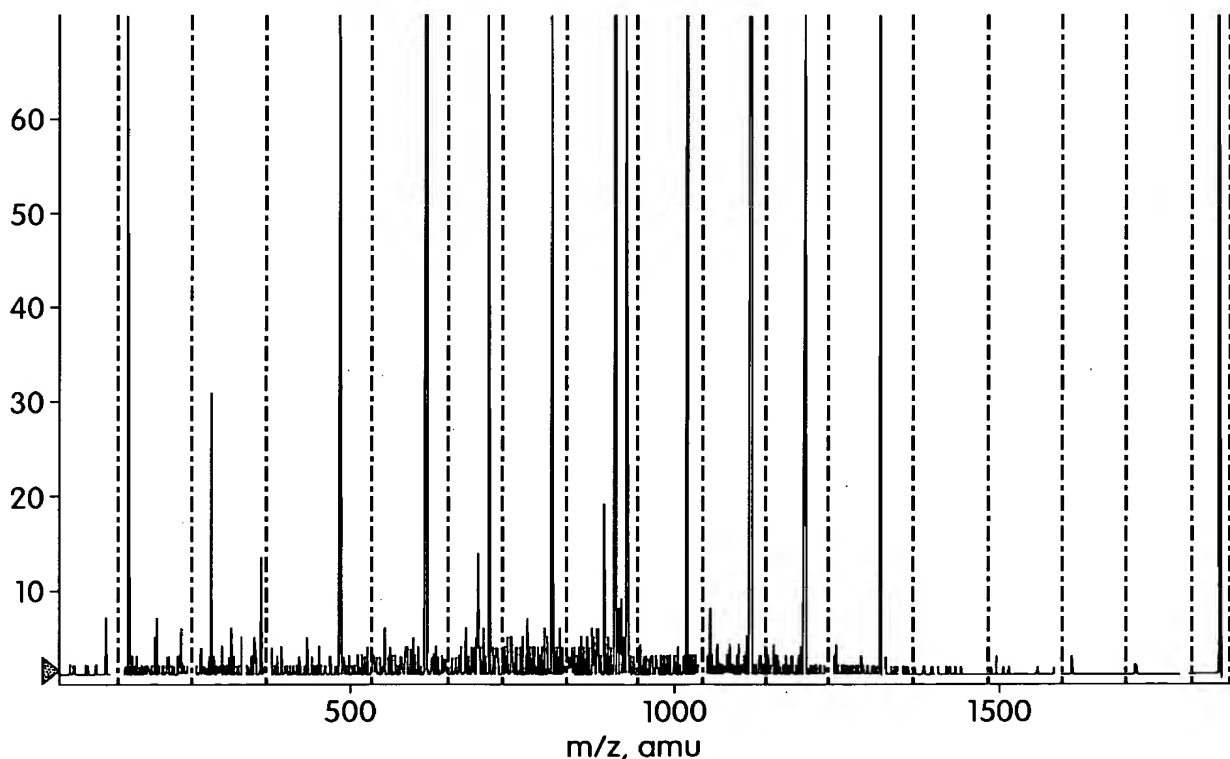


Fig. 3A

PEPTIDE 39 (NUM. HITS = 57)

(1.0) **VSALEVLPRD** (17.0)

SYMBOL	MASS	a	a - 17	b	b - 17	y	y - 17
V, Val	99.068	72.081	55.079	100.076	83.074	1098.616	1081.613
S, Ser	87.032	159.113	142.111	187.108	170.106	999.547	982.545
A, Ala	71.037	230.150	213.148	258.145	241.143	912.515	895.513
L, Leu	113.084	343.235	326.232	371.229	354.227	841.478	824.476
E, Glu	129.043	472.277	455.274	500.272	463.269	726.394	711.392
V, Val	99.068	571.346	554.343	599.340	582.338	599.352	582.349
L, Leu	113.084	684.430	667.427	712.424	695.422	500.283	483.281
P, Pro	97.053	781.482	764.480	809.477	792.475	387.199	370.196
D, Asp	115.027	896.509	879.507	924.504	907.502	290.146	273.144
R, Arg	156.101	1052.610	1035.608	1080.605	1063.603	175.119	158.117

+TOF PRODUCT: FROM 549.3

2.15e2

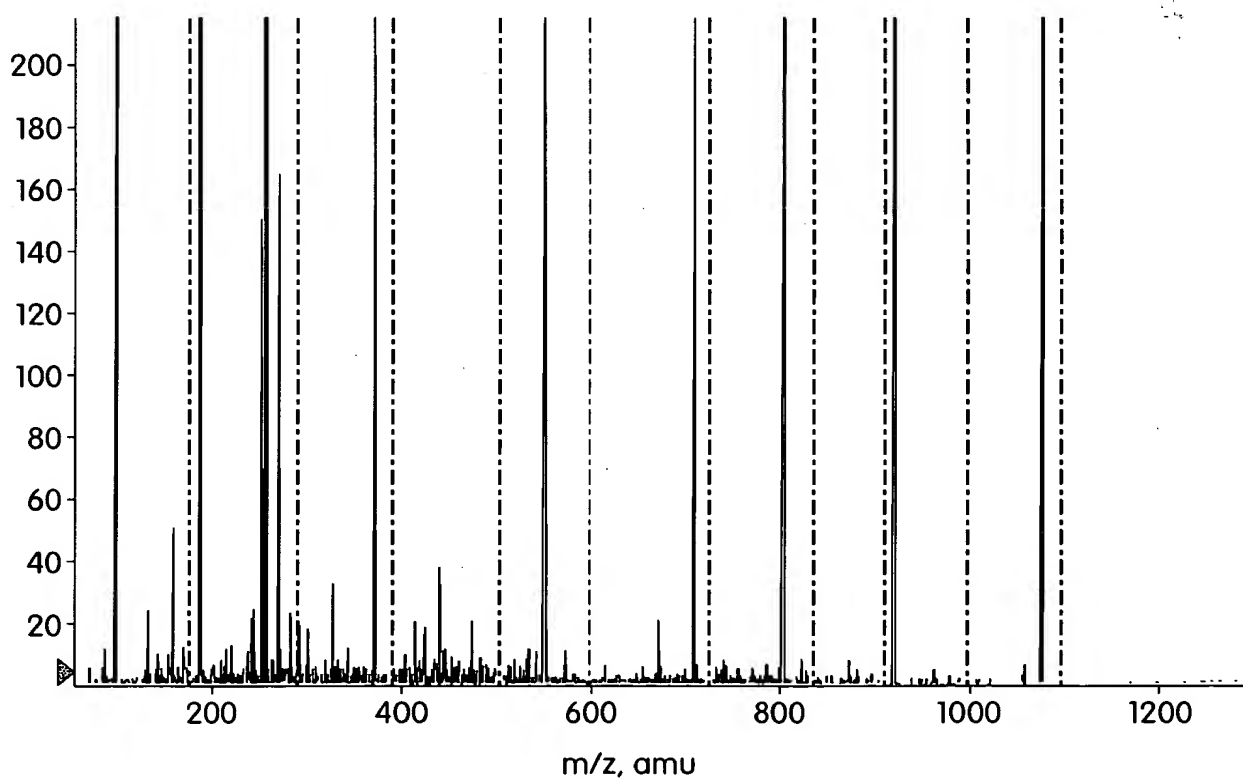


Fig. 3B

PEPTIDE 69 (NUM. HITS = 59)

(1.0) LVTDEDVFPTK

(17.0)

SYMBOL	MASS	a	a - 17	b	b - 17	y	y - 17
L, Lue	113.084	86.097	69.094	114.092	97.089	1263.647	1246.645
V, Val	99.068	185.165	168.163	213.160	196.158	1150.563	1133.560
T, Thr	101.048	286.213	269.210	314.208	297.205	1051.495	1034.492
D, Asp	115.027	401.240	384.237	429.235	412.232	950.447	933.444
E, Glu	129.043	530.283	513.280	558.277	541.275	835.420	818.418
D, Asp	115.027	645.310	628.307	673.304	656.302	706.378	689.375
V, Val	99.068	744.378	727.375	772.373	755.370	591.351	574.348
F, Phe	147.068	891.446	874.444	919.441	902.439	492.282	475.279
P, Pro	97.053	988.499	971.496	1016.494	999.491	345.214	328.211
T, Thr	101.048	1089.547	1072.544	1117.542	1100.539	248.161	231.158
K, Lys	128.095	1217.642	1200.639	1245.637	1228.634	147.113	130.111

+TOF PRODUCT: FROM 632.3

8.60e1

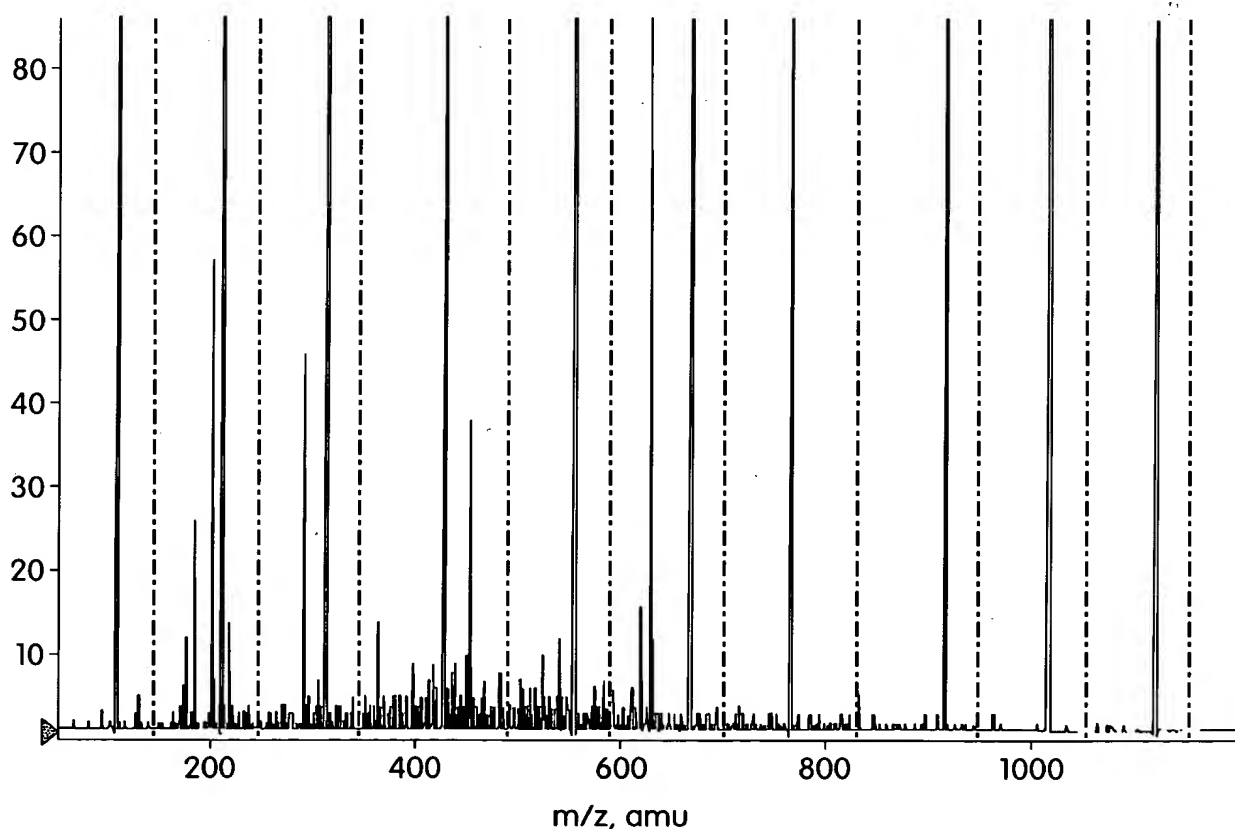


Fig. 4A

PEPTIDE 71 (NUM. HITS = 59)

(1.0) EFPSSFESLVR

(17.0)

SYMBOL	MASS	a	a - 17	b	b - 17	y	y - 17
E, Glu	129.043	102.056	85.053	130.050	113.048	1297.643	1280.640
F, Phe	147.068	249.124	232.121	277.119	260.116	1168.600	1151.597
P, Pro	97.053	346.177	329.174	374.172	357.169	1021.532	1004.529
S, Ser	87.032	433.209	416.206	461.204	444.201	924.479	907.476
S, Ser	87.032	520.241	503.235	546.236	531.233	837.447	820.444
F, Phe	147.068	667.309	650.307	695.304	678.301	750.415	733.412
E, Glu	129.043	796.352	779.349	824.347	807.344	603.346	586.344
S, Ser	87.032	883.384	866.381	911.379	894.376	474.304	457.301
L, Leu	113.084	996.468	979.465	1024.463	1007.460	387.272	370.269
V, Val	99.068	1095.536	1078.534	1123.531	1106.528	274.188	257.185
R, Arg	156.101	1251.637	1234.635	1279.632	1262.630	175.119	158.117

+TOF PRODUCT: FROM 649.4

4.50e1

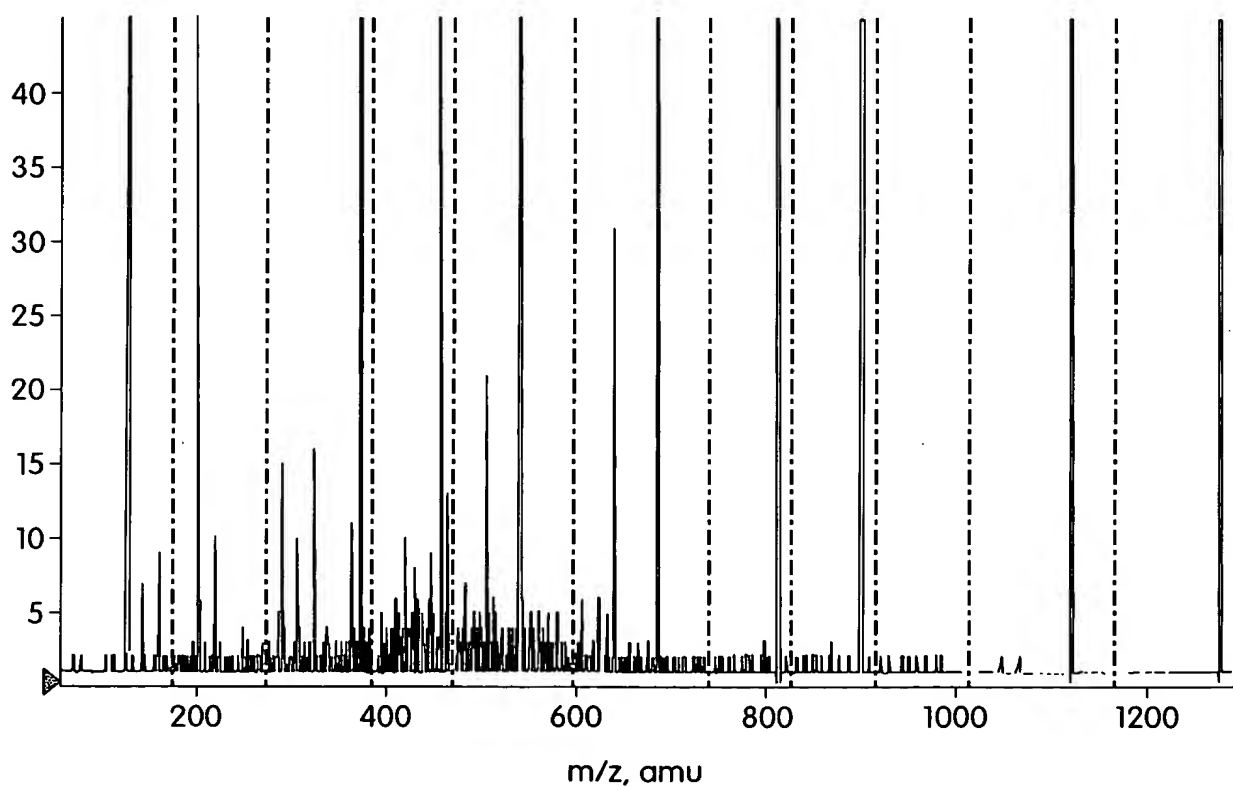


Fig. 4B

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1   MRKETPPPLV PPAAREWNLP PNAPACMERQ LEAARYRSDG ALLLGASSLS
51  GRCWAGSLWL FKDPCAAPNE GFCSAGVQTE AGVADLTWVG ERGILVASDS
101 GAVELWELDE NETLIVSKFC KYEHDDIVST VSVLSSGTQA VSGSKDICIK
151 VWDLAQQVVL SSYRAHAAQV TCVAASPHKD SVFLSCSEDN RILLWDTRCP
201 KPASQIGCSA PGYLP TSLAW HPQQSEVFVF GDENGTVSLV DTKSTSCVLS
251 SAVHSQCVTG LVFSPHSVPF LASLSEDCSL AVLDSSLSEL FRSQAHRDFV
301 RDATWSPLNH SLLTTVGWDH QVVHHVVPTE PLPAPGPASV TE

```

Fig. 5

Protein Translation of MOB-related protein EST GI 705582

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1   HHLGVLHRRD VSDDGRVHNK YYWYDERGKK VKCTAPQYVD FVMSSVQKLV TDEDVFPTKY
61  GREFPSSFES LVRKICRHLF HVLAH

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MOB-related Hypotetical Protein GI 8922671

```

1   MSFLFSSRSS KTFKPKKNIP EGSHQYELLK HAEATLGSGN LRQAVMLPEG EDLNEWIAVN
61  TVDFFNQINM LYGTITEFCT EASCPVMSAG PRYEYHWADG TNIKKPIKCS APKYIDYLMT
121 WVQDQLDDET LFPSKIGVPF PKNFMSVAKT ILKRLFRVYA HIYHQHFDSV MQLQEGAHLN
181 TSFKHFIFV QEFNLIDRRE LAPLOELIEK LGSKDR

```

Spindlin GI 5730065

```

1   MQAMLEVSAN MMKKRTSHKK HRSSVGPSKP VSQPRRNIVG CRIQHWKEG NGPVTQWKGT
61  VLDQVPVNPS LYLIKYDGFD CVYGLELNKD ERVSALEVL DRVATSRISD AHLADTMIGK
121 AVEHMFETED GSKDEWRGMV LARAPVMNTW FYITYEKDPV LYMYQLLDDY KEGDLRIMPD
181 SNDSPPAERE PGEVVD SLVG KQVEYAKEDG SKRTGMVIHQ VEAKPSVYFI KFDDDFHIYV
241 YDLVKTS

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Fig. 6

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		*	20	*	40	
gi3342738	:	-----		-----		-
gi10435124	:	-----		-----		-
EST705582	:	-----		-----		-
gi11414881	:	-----		-----		-
gi10432886	:	-----		-----		-
gi10435207	:	-----		-----		-
gi8922671	:	-----		-----		-
ScMob1	:	MSFLQNFHISPGQTIRSTRGFKWNTANAANNAGSVSPTKAT				41
spMob1	:	-----		-----		-

		*	60	*	80	
gi3342738	:	-----		-----		-
gi10435124	:	-----		-----		-
EST705582	:	-----		-----		-
gi11414881	:	-----		-----		-
gi10432886	:	-----		-----		-
gi10435207	:	-----		-----		-
gi8922671	:	-----		-----		-
ScMob1	:	PHNNTINGNNNNANTINNRADFTNNPVNGYNESDHGRMSPV				82
spMob1	:	-----		-----		-

		*	100	*	120	
gi3342738	:	-----	KSRRAGVTKMSNPFLKQVFENKDK	-----	FRPKRKFEPCIQ	36
gi10435124	:	-----	MS-IALKQVFENKDK	-----	FRPKRKFEPCIQ	26
EST705582	:	-----		-----		-
gi11414881	:	-----	MDWLMGKSKAKPNGKKPAAEER	-----		22
gi10432886	:	-----	MSELLSRSSKFFKPKNIPEGSH	-----		24
gi10435207	:	-----	MSELLSRSSKFFKPKNIPEGSH	-----		24
gi8922671	:	-----	MSELLSRSSKFFKPKNIPEGSH	-----		24
ScMob1	:	LTTPKRHAPPPEQLQNVTDENYTPSHQKPELQPOAGTTVIT				123
spMob1	:	-----	MEGFSNKTAKFERVRK-TEAGTK	-----		22

k f

		*	140	*	160	
gi3342738	:	-----	RPEELHCKAQAASLNAGLDLRLAVOLPPGEDNDWVAVHVVD	-----	DF	77
gi10435124	:	-----	RPEELHCKAQAASLNSGVLDLAAVOLPPSGEDNDWVAVHVVD	-----	DF	67
EST7.5582	:	-----		-----		-
gi11414881	:	KAYDEPEHTKARITDFOFKELVVLPREIDNEWLASNTTF				63
gi10432886	:	QVEELKHAEATLGS-CNLROAVMLPEGEDNEWIAVNEVD				64
gi10435207	:	QVEELKHAEATLGS-CNLROAVMLPEGEDNEWIAVNEVD				64
gi8922671	:	QVEELKHAEATLGS-CNLROAVMLPEGEDNEWIAVNEVD				64
ScMob1	:	HQDIKQIVEMTLGSEGVLNQAVKLPRGEDNEWLAVHCVDF				164
spMob1	:	HYOLROYAEATLGS-CSLMEAVKLPRGEDNEWIAMNEMDF				62

1 1 av lp ged n w a df

Fig. 7

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      *           180           *           200
gi3342738 : FNRVNLIYGTISDGCTEQSCPVMSCGPKYEYRWODEHKFRK : 118
gi10435124 : FNRINLIYGTICEFCTERTCPVMSGPKYEYRWODDLKYRK : 108
EST705582 : -HHLGVLR-----RDVSDDG-RVHN-KYYWYDER--GK : 29
gi11414881 : FHHINLQYSTISEFCTGETCOTM-AVCNTQYYWYDER--GK : 101
gi10432886 : FNCINMLYGTITEFCTEASCPVMSAGPRYEYHWADGTNIRK : 105
gi10435207 : FNCINMLYGTITEFCTEASCPVMSAGPRYEYHWADGTNIRK : 105
gi8922671 : FNCINMLYGTITEFCTEASCPVMSAGPRYEYHWADGTNIRK : 105
ScMob1 : YNCINMLYGSITEFCSPQTCPRMIAITNEYEYLWAFQK-GQP : 204
spMob1 : YTCINMLYGTITEFCTAASCPQMNAGPSYEYVWQDDKIYTK : 103
      6n6 yg i efc cp m y Y W d k

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      *           220           *           240
gi3342738 : PTALSAPRYMDLLMWIEAQINNEDLFPTNVGTPFDKQNFQ : 159
gi10435124 : PTALPAPOYMNLLMWIEVQINNEEIFPTCVGVFPKQNFQ : 149
EST705582 : KVKCTAPOYVDEVMSSVQKLVTDEDVFPTKYGREFPSSFES : 70
gi11414881 : KVKCTAPOYVDEVMSSVQKLVTDEDVFPTKYGREFPSSFES : 142
gi10432886 : PTKCSAPKYIDYLMFWVQDOLDDETLFPSKIGVFPKQNFMS : 137
gi10435207 : PTKCSAPKYIDYLMFWVQDOLDDETLFPSKIGVFPKQNFMS : 146
gi8922671 : PTKCSAPKYIDYLMFWVQDOLDDETLFPSKIGVFPKQNFMS : 146
ScMob1 : PVSVSAPKYVECLMRWCQDQEDDESIFPSKYTGTFPEGFQ : 245
spMob1 : PTRMSAPDYINNLLDWIQEKLDDKKLFPTTEIGVEFPKQNRK : 144
      p AP Y6 66 w 2 1e 6FP3 g fp f

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      *           260           *           280
gi3342738 : -TVRKILSRLEFVTVHVYIHHFDRTAOMGSEAHVNTCYGHF : 199
gi10435124 : -ICKKILCRLEFVTVHVYIHHFDRVTVMGATAHVNTCYGHF : 189
EST705582 : -LVRKICRHLFHVLAH----- : 85
gi11414881 : -LVRKICRHLFHVLAHIYWAHFKETALELHGILNTLYVHF : 182
gi10432886 : -----ELTILSKYSF : 146
gi10435207 : -VAKTILCRLEFVVAHIYHQHFDSVMLOQEAHLNTSEKHF : 186
gi8922671 : -VAKTILCRLEFVVAHIYHQHFDSVMLOQEAHLNTSEKHF : 186
ScMob1 : RVIQPIERRLFRVAHIYCHHFNEELNLOTVLNTSEKHF : 286
spMob1 : -VLOQIERRLFRVAHIYCSHFHVVAAMELISYLNNTSEKHF : 184
      i lf h y hf nt hf

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      *           300           *           320
gi3342738 : YMFVKEEGLIIDTKLEPLVRGLGAEGVRNHQVRHLEPPGEG : 240
gi10435124 : YMFVTENMLIDRKLEPL----- : 206
EST705582 : ----- : -
gi11414881 : ILFARENNLLDPKETA----- : 199
gi10432886 : F----- : 148
gi10435207 : IFVQEEENLIERRRELAP----- : 203
gi8922671 : IFVQEEENLIERRRELAP----- : 203
ScMob1 : CLFAQEEELIRPADFG----- : 303
spMob1 : VRECREEGLMENKEYAP----- : 201
      f e l

```

Fig. 7 Cont.

	*	340	*	360	
gi3342738	:	PPSRAIKET	HEIRNCLMKCISLYLEDEAQ	TPTPLSPPGLGM	: 281
gi10435124	:	-----	IKEMTS-RMCH	-----	: 216
EST705582	:	-----	-----	-----	: -
gi11414881	:	-----	MDDLTEVLC	CSGAGGVHSGGSGDGAGSGGPGAQNHVK	: 235
gi10432886	:	-----	-----	-----	: -
gi10435207	:	-----	LOELIEK	GSKDR	: 216
gi8922671	:	-----	LOELIEK	GSKDR	: 216
ScMob1	:	-----	LEELVME	RDR	: 314
spMob1	:	-----	MDLVDSMV	-----	: 210

	*	
gi3342738	:	SPAARPRSFP : 291
gi10435124	:	----- : -
EST705582	:	----- : -
gi11414881	:	ER----- : 237
gi10432886	:	----- : -
gi10435207	:	----- : -
gi8922671	:	----- : -
ScMob1	:	----- : -
spMob1	:	----- : -

Fig. 7 Cont.

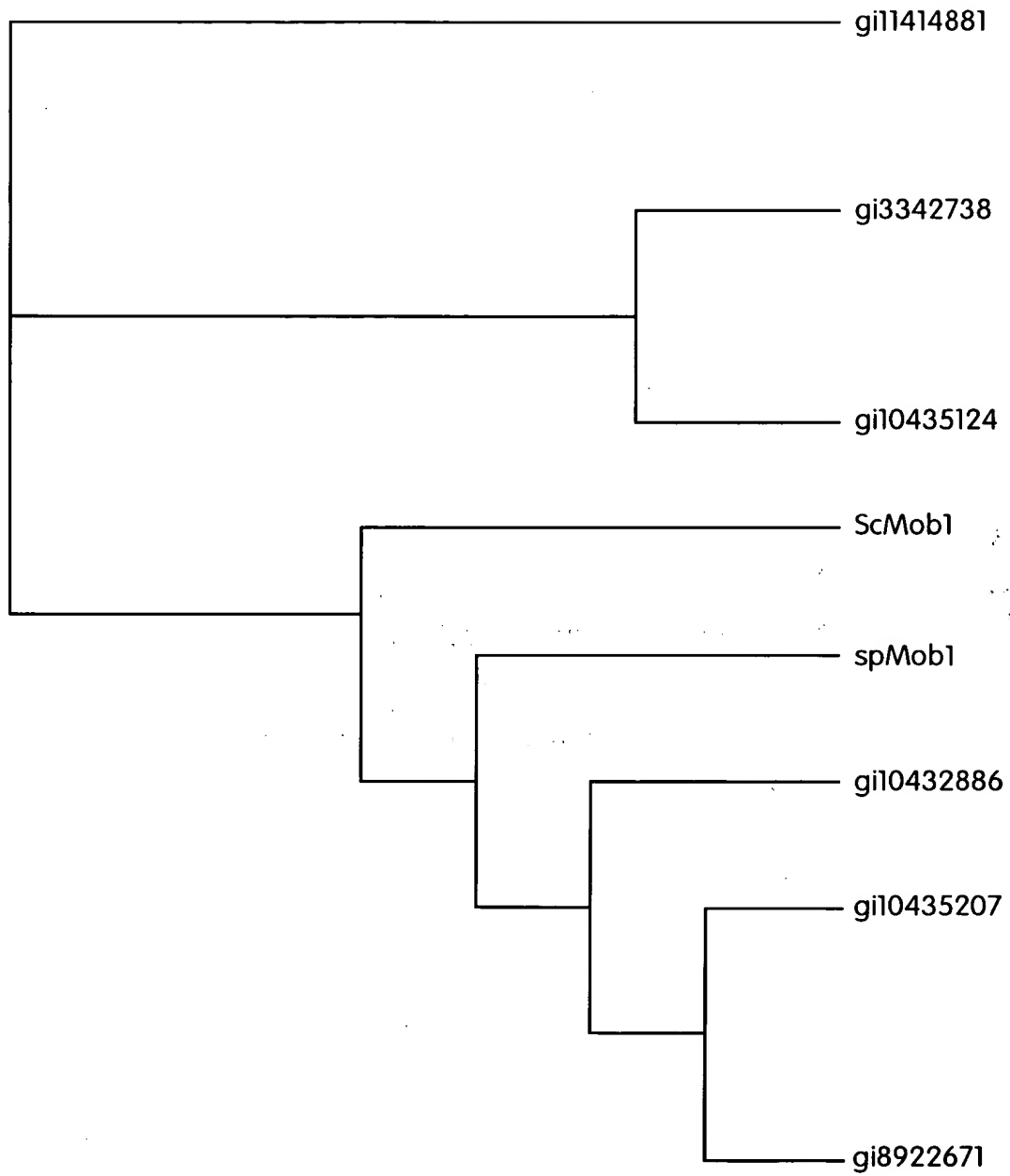


Fig. 8

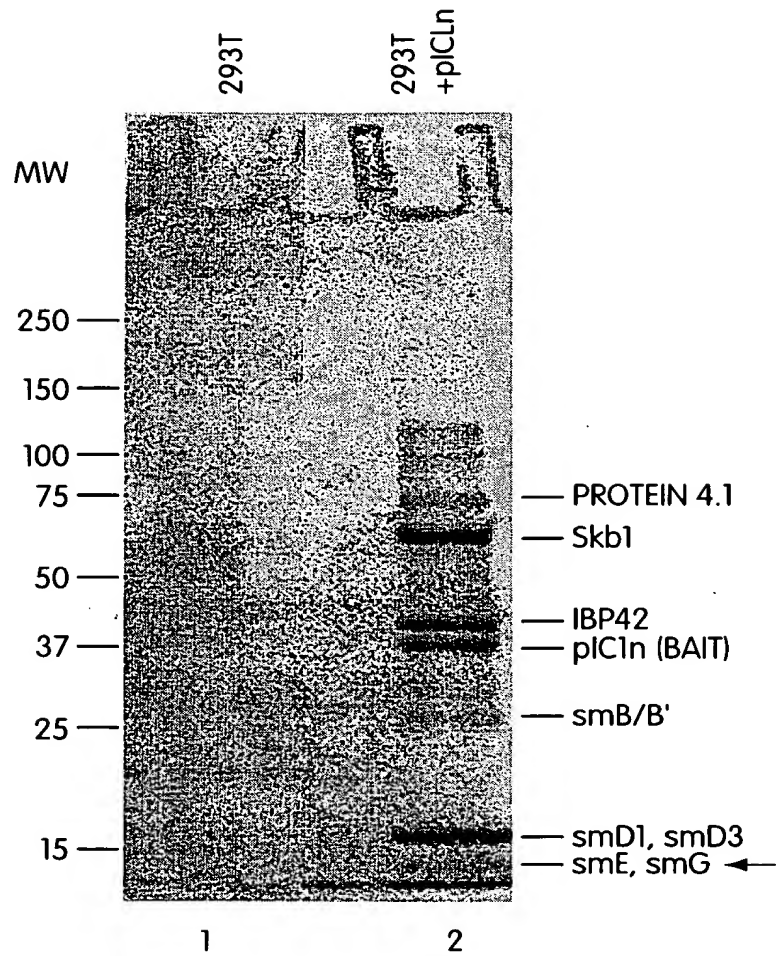


Fig. 9

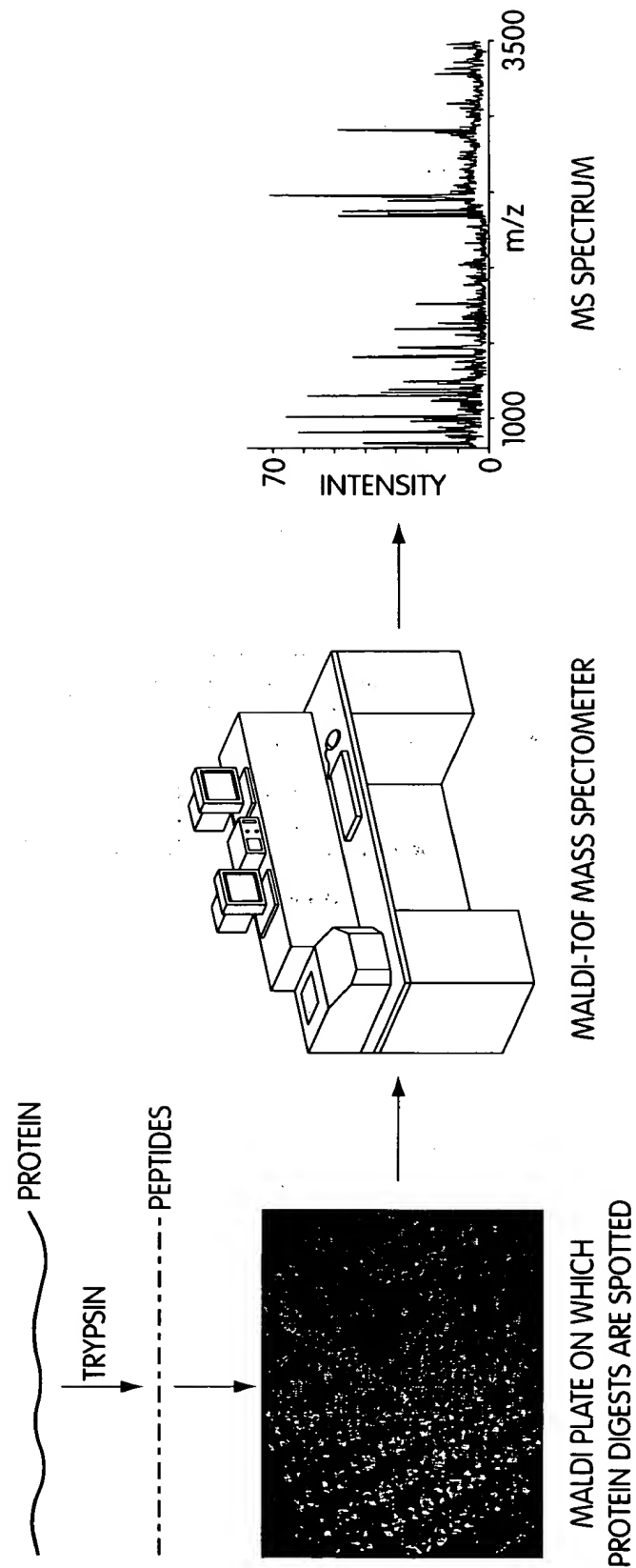


Fig. 10

1. EXCISE THE SPOT/BAND OF INTEREST, CUT THE FRAGMENT INTO SMALLER PIECES.
2. SHRINK THE GEL PIECES IN ACETONITRILE FOR APPROX. 10 MIN. REMOVE EXCESS ACETONITRILE, AND DRY UNDER VACUUM WITH CENTRIFUGATION (SpeedVac).
3. COVER GEL PIECES WITH 10mM DITHIOTHREITOL (DTT) IN 50-100mM NH_4HCO_3 .
4. COOL TO ROOM TEMP, REMOVE DTT SOLUTION AND ADD EQUAL VOLUME OF 55 mM IODOACETAMIDE IN 50-100 mM NH_4HCO_3 . INCUBATE FOR 45 MIN IN DARK WITH OCCASIONAL STIRRING.
5. RINSE THE GEL WITH 50-100 μL ALIQUOTS OF 50-100 mM NH_4HCO_3 FOR 10 MIN AND REMOVE EXCESS.
6. SHRINK THE GEL WITH ACETONITRILE FOR 10 MIN AND REMOVE EXCESS.
7. SWELL THE GEL WITH 50-100 mM NH_4HCO_3 , AND SHRINK AGAIN WITH ACETONITRILE.
8. REMOVE EXCESS LIQUID AND DRY DOWN USING A SpeedVac.
9. SWELL GEL PIECES AT 4°C FOR 45 MIN IN BUFFER CONTAINING TRYPSIN AND 50 mM NH_4HCO_3 . (APPROX. 5 $\mu\text{L}/\text{mm}^2$ GEL). THE GEL PIECES SHOULD JUST BE COVERED. (TRYPSIN SOLUTION AT 12.5 ng/ μL IS TYPICALLY USED FOR SILVER STAINED GELS).
10. DIGEST OVERNIGHT AT 37°C (OR AT LEAST FOR 3 H).
11. CENTRIFUGE GEL PIECES AND COLLECT SUPERNATANT
12. FURTHER EXTRACT PEPTIDES BY ONE CHANGE OF 20 mM NH_4HCO_3 FOLLOWED BY CENTRIFUGATION AND POOL SUPERNATANT.
13. FURTHER EXTRACT WITH THREE CHANGES OF 5% FORMIC ACID IN 50% CH_3CN (20 MIN BETWEEN CHANGES) AT ROOM TEMP.
14. DRY SAMPLE DOWN IN SpeedVac UNTIL DESIRED VOLUME HAS BEEN REACHED OR TO DRYNESS.

Fig. 11

DESALTING:

1. THE SAMPLE (STEP 14 IN TABLE 1.0) SHOULD BE EITHER **a)** RESUSPENDED IN 5% (v/v) METHANOL AND 5% (v/v) FORMIC ACID OR **b)** AT LEAST ACIDIFIED BY THE ADDITION OF FORMIC ACID.
2. WASH ZipTips (MILLIPORE) BY PIPETTING IN AND OUT OF THE TIP THREE ALIQUOTS OF 60% (v/v) METHANOL AND 5% (v/v) FORMIC ACID SOLUTION.
3. EQUILIBRATE THE TIPS WITH 5% (v/v) METHANOL AND 5% (v/v) FORMIC ACID.
4. EXTRACT THE ANALYTES FROM THE SAMPLE BY PIPETTING IT UP AND DOWN 10 TO 20 TIMES.
5. WASH THE TIP WITH A SOLUTION OF 5% (v/v) METHANOL AND 5% (v/v) FORMIC ACID.
6. ELUTE THE ANALYTES OFF THE TIP USING (3 μ l) OF A SOLUTION OF 60% (v/v) METHANOL AND 5% (v/v) FORMIC ACID.

APPLICATION TO MALDI PLATE:

1. PREPARE A FRESH SATURATE SOLUTION OF α -CYANO-4-HYDROXY-CINNAMIC ACID (DOUBLY RE-CRYSTALLIZED) IN 50% (v/v) ACETONITRILE 0.3% (v/v) TRIFLUOROACETIC ACID.
2. TAKE 0.5 μ l OF SAMPLE (ELUENT IN STEP 6 OF THE DESALTING PROTOCOL) AND PIPET ONTO ONE POSITION ON THE MALDI PLATE.
3. IMMEDIATELY ADD 0.5 μ l OF THE SATURATE MATRIX SOLUTION (FROM STEP 1) AND ALLOW TO AIR DRY FOR AT LEAST 5 MINUTES.
4. REPEAT THE PROCESS FOR ALL SAMPLES.
5. INSTALL THE PLATE IN THE MALDI-TOF MS.

Fig. 12



Fig. 13A

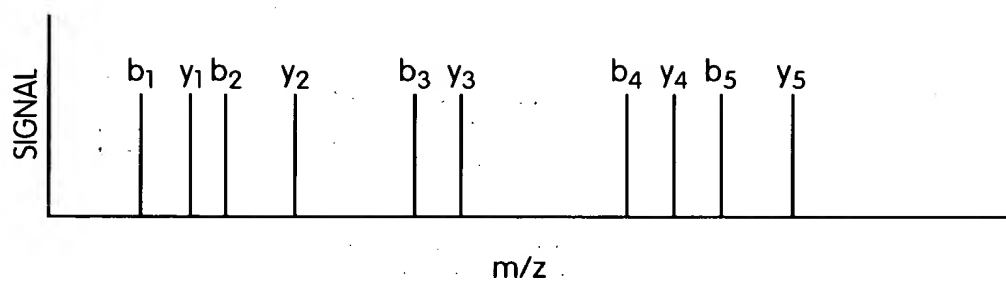


Fig. 13B

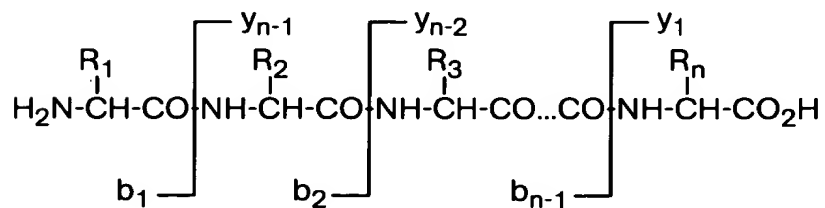
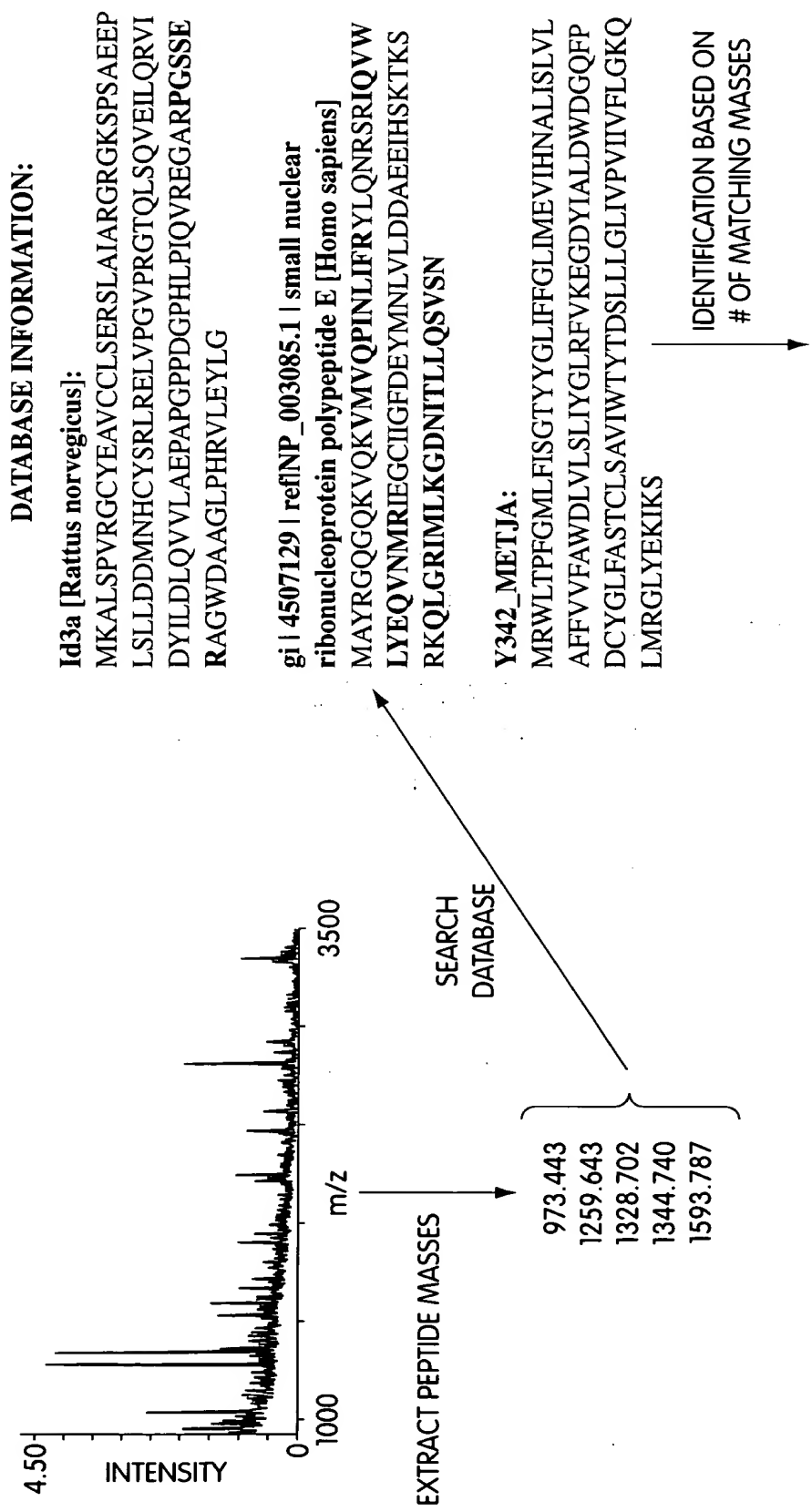


Fig. 13C



PROTEIN IDENTITY: SMALL NUCLEAR RIBONUCLEOPROTEIN POLYPEPTIDE E (smE)

Fig. 14

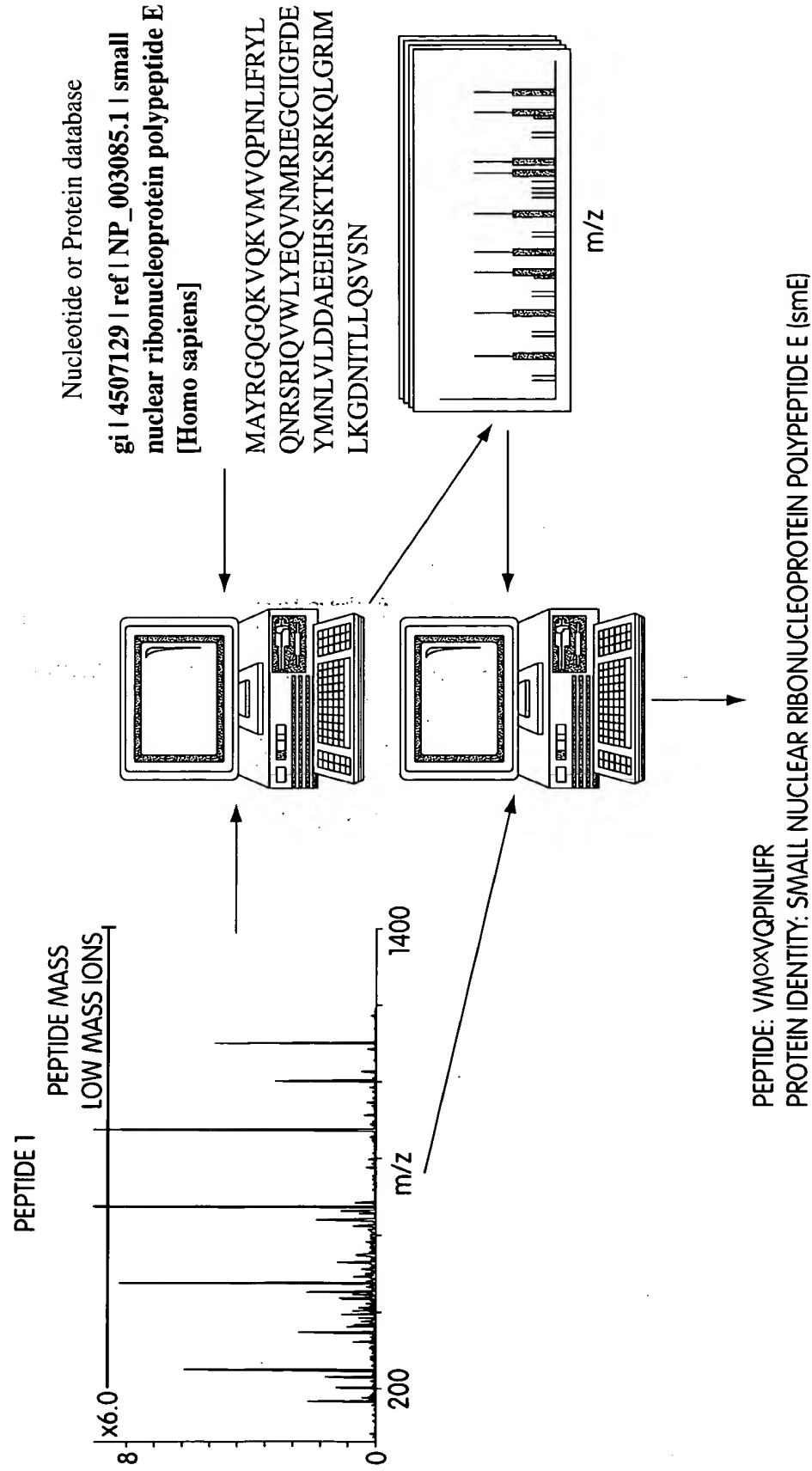


Fig. 15

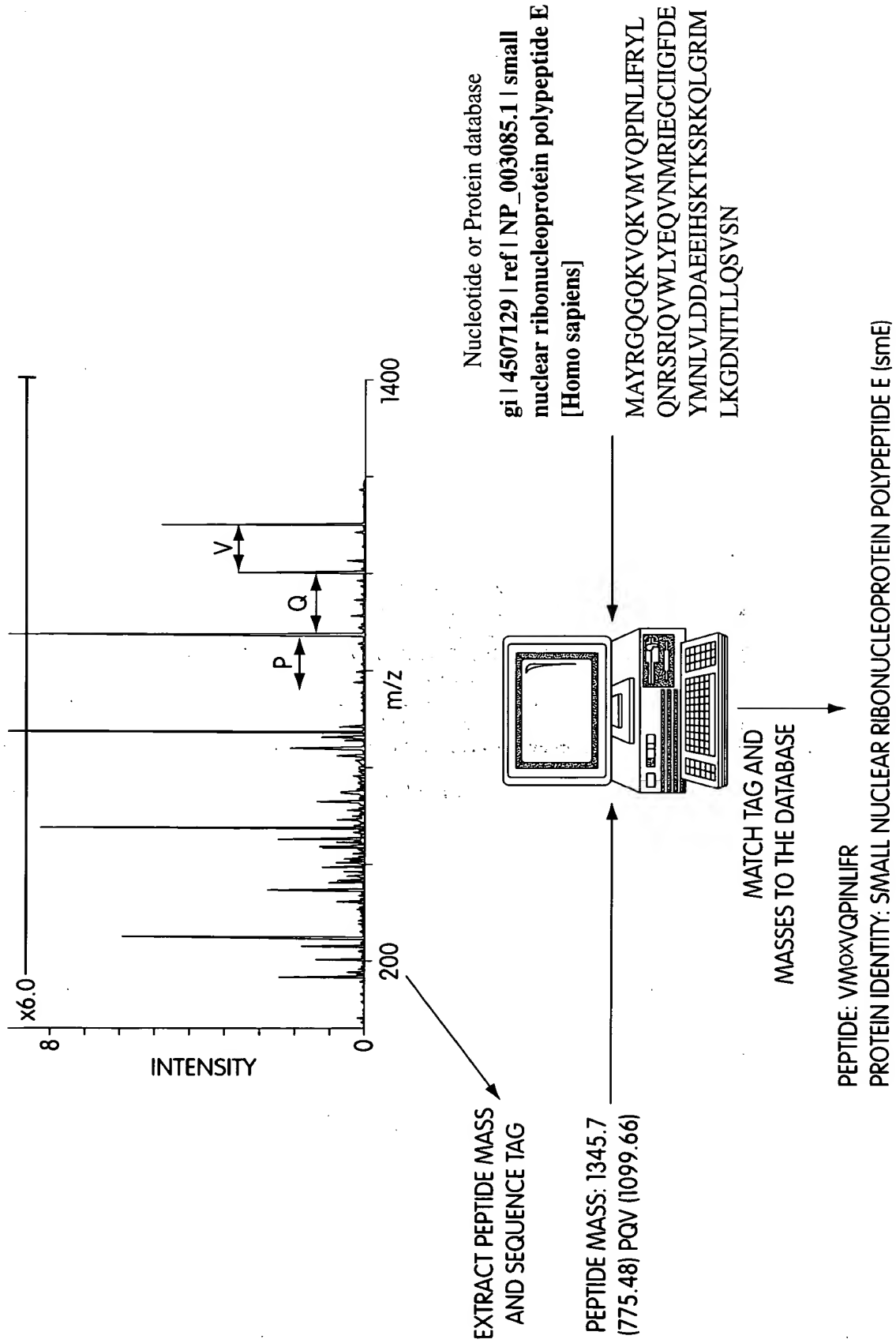
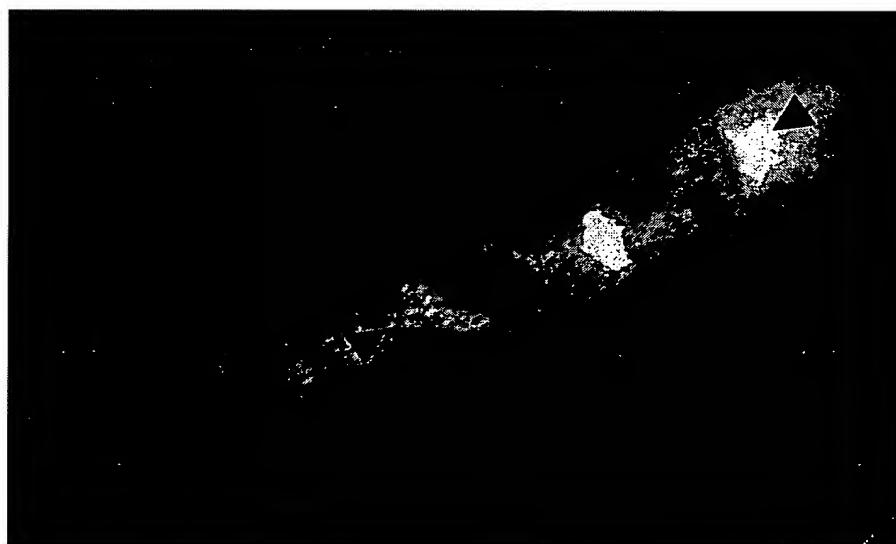


Fig. 16



PHASE CONTRAST

Fig. 17A



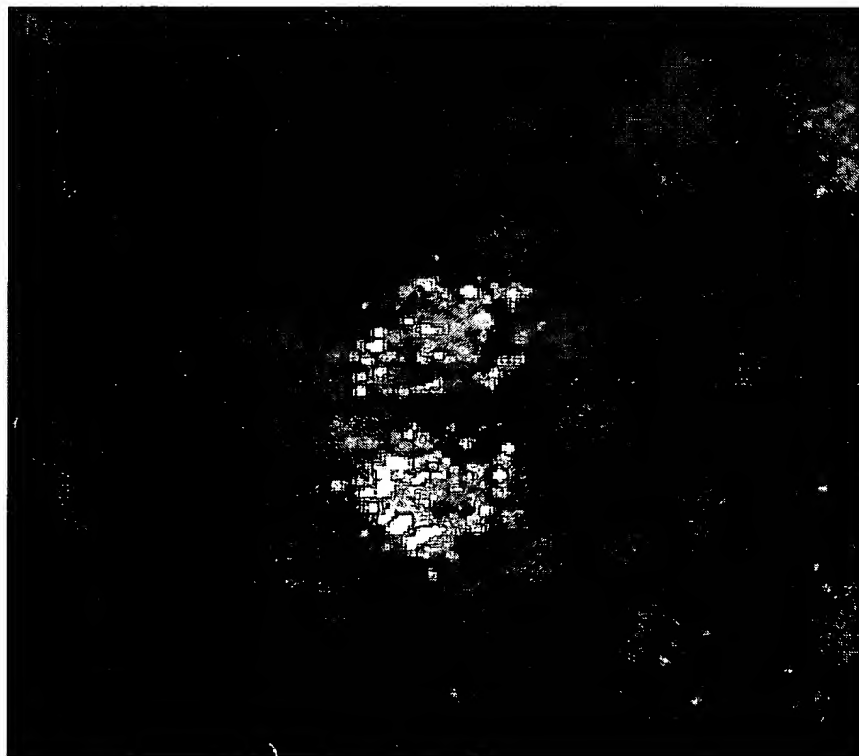
N-FLAG/Skb1

Fig. 17B



PHASE CONTRAST

Fig. 18A



ENDOGENOUS Skb1

Fig. 18B

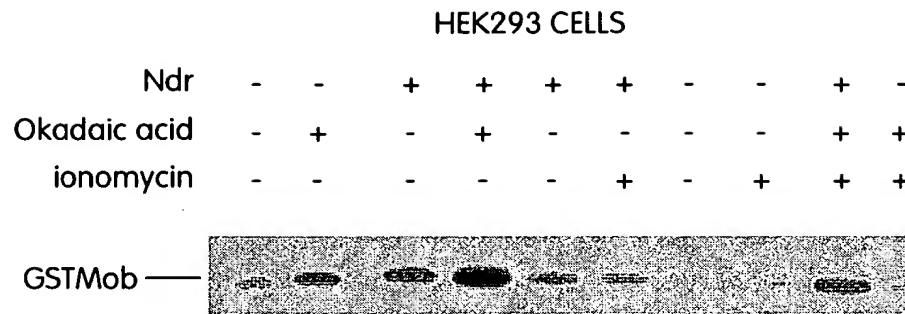


Fig. 19A

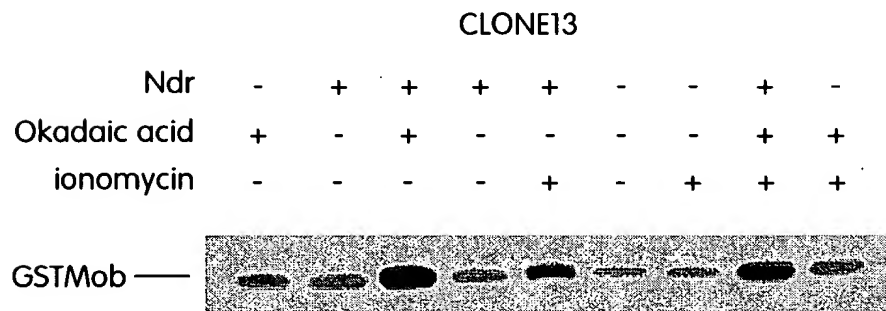


Fig. 19B

	*	20	*	40	
gi13543922	:	-----	:	-----	:
AF258661	:	-----	:	-----	:
sudD	:	-----	:	-----	:
RIO1	:	-----	:	-----	:
HssudD	:	MDLVGVASPEPGTAAAWGPSKCPWAIPQNTISCSLADVMSE	:		41
FLJ11159	:	-----	:	-----	:

	*	60	*	80	
gi13543922	:	-----	:	-----MSRVV	5
AF258661	:	-----	:	-----	-
sudD	:	-----	:	-----MSSDSTTQA	9
RIO1	:	-----	:	-----	-
HssudD	:	QLAKELQLEEEAAVFPEVAVAEGPFITGENIDTSSDLMLAQ	:		82
FLJ11159	:	-----	:	-----MGKVVNV	6

	*	100	*	120	
gi13543922	:	PGQFDDADSSDSENRLKTVKEKDDILFEDLQDNVNENEGE	:		46
AF258661	:	-----	:	-----	-
sudD	:	ASPAEGLNPSHTYVPNKGYANEDGAVPAMAGQDLTPEDEDY	:		50
RIO1	:	-----	:	-----	-
HssudD	:	MLQMEYDREYDAQLRREEKKFNGDSKVSISFENYRKVHPYE	:		123
FLJ11159	:	AKLRYMSRDDFRVLTAVEMGMKNHEIVPGSLIASIASLKHG	:		47

	*	140	*	160	
gi13543922	:	EIEDEEEEGYDDDDDDWDWDEG-VGKLAKGYVWNGGSNPQA	:		86
AF258661	:	-----	:	-----	-
sudD	:	EGDEYYDDIFEEELDEGDFNSSNPADLTAKAYNRQRRVNELA	:		91
RIO1	:	-----	:	-----	-
HssudD	:	DSDSSEDEVDWQDTRDDPYRPAKPVPTPKKGFIGKGDITT	:		164
FLJ11159	:	GCNKVLRELVKHKLIAWERTKTVQGYRLTNAGYDYLALKTL	:		88

	*	180	*	200	
gi13543922	:	NRQTSDDSSAKMSTPADKVLRRKFENKINLDKLNVTDSVIN	:		127
AF258661	:	-----	:	-----	-
sudD	:	ADPNAPKWITYPKTNTQKPTVNTYASVDDEIKSLTRHAAKI	:		132
RIO1	:	-----MSLEDKFDSLVSQASDHINNQLLEKYSHKIK	:		33
HssudD	:	KHDEVVCGRKNTARMENFAPEFQVGDGIGMDLKLNSNHVFNA	:		205
FLJ11159	:	SSRQVVESVGNQMGVKGESDIYIVANEEGQQFALKLHRLG	:		129

Fig. 20


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      *           220           *           240
gi13543922 : VTEKSRQKEADMYRIKD KADRAIVEQVLDPRIRMI LFKMIT : 168
AF258661   : ----- : -
sudD       : LDNVQSGLA VRGGSGTDRADRAISEQVLDPRIRMI LLOMEN : 173
RIO1       : TDELSFS---RAKTSKD KANRAIVENVLDPRIRMF LKSMVT : 71
HssudD     : LKQHAYSEERRSARLHEKKEHS LAEKAVDPKIRLLMYKMAN : 246
FLJ11159   : TSFRNLKKNRKYHRYHNVSWLYLSRI SAMKEFAYMKALYE : 170

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      *           260           *           280
gi13543922 : RGIITEINGGISICKKEANVYIAST----- : 192
AF258661   : ----- : -
sudD       : RNLVSEIHCGLSICKKEANVYHAMLQP-----E : 200
RIO1       : RGVHADLNGCLSLICKKEANVYHAFAGTGKAPVIDEETGQYEV : 112
HssudD     : SGMLETITGCLSLICKKEANVYHAYGGSMED-----EK : 277
FLJ11159   : RKFPVPKP--IDYNRHAVVMELING-----Y : 194

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v

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      *           300           *           320
gi13543922 : ----ANGESRAIKLYKTSILVFKDRDKAVSGEERFRHGYCK : 229
AF258661   : ----- : -
sudD       : DDFDAAPIHRAIKVYKTSILVFKDRDKAVTGEERFRSGYNK : 241
RIO1       : LETDGSRAEYAIKLYKTSILVFKDRDKAVDGEERFRNSRSQ : 153
HssudD     : EDSKVIPTCAIKVFKTSILNFKDRDKAVKDDERFKDRFSK : 318
FLJ11159   : PLCQIHVEDPASVYDEAMEIVKLANHGLIHGDENEFNLI : 235

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f

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      *           340           *           360
gi13543922 : GNPRKMVKIWA EKEMNLIRLN-TAEIPCPEPIMLRSHVLV : 269
AF258661   : ----MVK IWA EKEMNLIRLN-TAEIPCPEPIMLRSHVLV : 35
sudD       : SNPRAMVKIWA EKEMNLRRIY-AAGIPCPEPINLRSHVLV : 281
RIO1       : HNPRKMIKIWA EKEFNLRRIYQSGVIPAPKITEVKNNVLV : 194
HssudD     : LNPRKIHRNWA EKEMNLARMO-RAGIPCPTVVLKKHILV : 358
FLJ11159   : LDES DHITVIDFPQMVSTSHPN--AEWYFDRDVKCIKDFFM : 274

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waek2m nl r a ip p 6 16

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      *           380           *           400           *
gi13543922 : MFEI GKDD-MPAPLLKNVQL----SESKARTELYOVIOYMR : 305
AF258661   : MSFI GKDD-MPAPLLKNVQL----SESKARTELYOVIOYMR : 71
sudD       : MGEVGN SKGTAAPRLKDVDFNISDPESKWRTELYDMLGYMR : 322
RIO1       : MEFLSRGNAFASPKLDYPIK---NRDEIFHYHTMVAYMR : 232
HssudD     : MSFI GHDO-MPAPKLKEVKLN----SEEMKEMAYQTLHMR : 394
FLJ11159   : KRFSYESE--LFPTFKDIRRE-----DTLDVEVSASGYTK : 307

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m F

P lK

y

ym4

Fig. 20 Cont.

		420	*	440	*	
gi13543922	:	RMVQDARLVH-ADLSEFNMLVHGCGVYIIDVSQSVEHDHPH	:	345		
AF258661	:	RMVQDARLVH-ADLSEFNMLVHGCGVYIIDVSQSVEHDHPH	:	111		
sudD	:	VMYQTCRLVH-ADLSEYNLIVHDDKLYVIDVSQSVEHDHPR	:	362		
RI01	:	ILYQVCRLVH-ADLSEYNLIVHDDKLYMIDVSQSVEPEHPM	:	272		
HssudD	:	QLYHECTLVH-ADLSEYNMLVHACKVWLIDVSQSVEPTHPH	:	434		
FLJ11159	:	EMQADDELLHPLGPDDKNVETKEGSEFSFSDGEVAEKAENVY	:	348		
		6y L6H adlse N h 5 idvs2svE hp				
		460	*	480	*	
gi13543922	:	ALEFLR-KDCANVN--DEFMRHSAVMT-VRELFEEVTDPS	:	382		
AF258661	:	ALEFLR-KDCANVN--DEFMRHSAVMT-VRELFEEVTDPS	:	148		
sudD	:	SLEFLR-MDIKNVS--DEFRKGVPTIS-ERVIFERI----	:	395		
RI01	:	SLEFLR-MDIKNVN--LYFEKMCISIFP-ERVIFQEVISET	:	309		
HssudD	:	GLEFLR-KDCRNVS--QFFQKGVKEALSRELFNAVSGLN	:	472		
FLJ11159	:	GSENESERNQLEESEGCYCRSSCDPEQIKEDSLSEESADAR	:	389		
		lefl 1 nv 5f r 6f				
		500	*	520	*	
gi13543922	:	ITHEN-MDAYISKAMEIASORTKEERSSQDHVDEEVFKRAY	:	422		
AF258661	:	ITHEN-MDAYISKAMEIASORTKEERSSQDHVDEEVFKRAY	:	188		
sudD	:	ISAEG-PATVTDELRDVAEKLFSLEPEAADEVDTAVERQOY	:	435		
RI01	:	LEKFKGDYNNISALVAYIASNLPIKSTEQDEADEEERSLH	:	350		
HssudD	:	ITADN-----EADFAEIEAEKMNEDHVKNGRKAAS	:	505		
FLJ11159	:	SFEMTEFNQAEIEIKGVVNNSVTEFSEEKNRTENNRQD	:	430		
		d				
		540	*	560	*	
gi13543922	:	TPRILNEVKNYERDMDIIMKLKEEDMAMNAQDNILYQTVT	:	463		
AF258661	:	TPRILNEVKNYERDMDIIMKLKEEDMAMNAQDNILYQTVT	:	229		
sudD	:	TPQLDQVYDYERDAEKVN-----AGEGDDLVR---	:	464		
RI01	:	TVRS-----	:	354		
HssudD	:	FLKDDGDPPLLYDE-----	:	519		
FLJ11159	:	GQRVQGGVPAGSDEYEDECPHLIALSSLNREFR-----	:	463		
		580	*	600	*	
gi13543922	:	GLKKDLSGVQKVPALLNQVEER-TCSDSEDIGSSECSDTD	:	503		
AF258661	:	GLKKDLSGVQKVPALLNQVEER-TCSDSEDIGSSECSDTD	:	269		
sudD	:	----DLLAREKPSAPPDDEAETGSEVSGGVSLAESGSEDEE	:	501		
RI01	:	-----	:	-		
HssudD	:	-----	:	-		
FLJ11159	:	----PFRDEENVGAMNQYRTRTLSITSGSAVSCSTIPPEL	:	500		

Fig. 20 Cont.

	620	*	640	*	
gil3543922	:	SEEQGDHARPKKHTTDPDIDKKERKKM	KEAQREKRKNK	:	544
AF258661	:	SEEQGDHARPKKHTTDPDIDKKERKKM	KEAQREKRKNK	:	310
sudD	:	ERDPFEKKPPRGKRFEDKESKKEHKNK	KEEKREKRANK	:	542
RI01	:	-----	-----	:	-
HssudD	:	-----	-----	:	-
FLJ11159	:	VKQKVKRQLTKQOKSAVRRRLQKGEAN	FTKORRENMONK	:	541

	660	*	
gil3543922	:	KHVKKRKEKTAKTKKGK	: 561
AF258661	:	KHVKKRKEKTAKTKKGK	: 327
sudD	:	KHVKKRLVSSSSSRKRK-	: 558
RI01	:	-----	: -
HssudD	:	-----	: -
FLJ11159	:	SSLEAASFWGE-----	: 552

Fig. 20 Cont.